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# Regional Resistance Surveillance Program Results for 12 Asia-Pacific Nations (2011)

**Rodrigo E. Mendes,[a] Myrna Mendoza,[b] Kirnpal K. Banga Singh,[c] Mariana Castanheira,[a] Jan M. Bell,[d] John D. Turnidge,[d] Stephen S. F. Lin,[e] Ronald N. Jones[a]**

JMI Laboratories, North Liberty, Iowa, USA[a]; Philippines General Hospital, Manila, Philippines[b]; Universiti Sains Malaysia, Kelantan, Malaysia[c]; School of Molecular and Biomedical Sciences, University of Adelaide, Adelaide, Australia[d]; Pfizer Inc., Shanghai, China[e]

**The Regional Resistance Surveillance program monitored susceptibility rates and developing resistance by geographic region, including 12 Asia-Pacific (APAC) countries. Reference broth microdilution methods for susceptibility/interpretations were applied, processing 5,053 strains. Among *Staphylococcus aureus* isolates (37% methicillin-resistant *S. aureus* [MRSA], highest in South Korea [73%]), linezolid (LZD), tigecycline (TIG), and vancomycin were 100% active, but 33 and 34% of strains were levofloxacin (LEV) or macrolide resistant, respectively. *Streptococcus pneumoniae* was most resistant to β-lactams and macrolides (45%) but was LZD, LEV, and TIG susceptible (>98%). Extended-spectrum β-lactamase (ESBL) phenotype rates in *Escherichia coli* and *Klebsiella* spp. were 48 and 47%, respectively, and were highest in Taiwan, at 75 to 91%. The best anti-ESBL-phenotype agents were amikacin (81 to 96% susceptible), colistin (COL; >98%), TIG (>98%), and carbapenems (81 to 97%). *Pseudomonas aeruginosa* showed ≥20% resistance to all drugs except COL (99% susceptible). In conclusion, endemic evolving antimicrobial resistances in APAC nations show compromised roles for many commonly used antimicrobials.**

The Regional Resistance Surveillance (RRS) program was organized in the Asia-Pacific (APAC) region to supplement sampling for four nations, China (reported separately), Indonesia, Philippines, and Thailand, for 2011. These 16 additional sampling sites contributed 100 to 250 isolates across specified Gram-positive and -negative pathogen groups to the SENTRY Antimicrobial Surveillance Program platform. Nine other nations were also sampled (Australia, Hong Kong, India, Japan, South Korea, Malaysia, New Zealand, Singapore, and Taiwan) with organisms referred to a central monitoring laboratory for reference (1, 2) testing against more than 30 antimicrobial agents and follow-up molecular procedures (3). The focus of the surveillance protocol was to recognize and quantitate the level of resistance to commonly used, generally older, cost-effective antimicrobials (4) and, where possible, to characterize the resistance mechanisms.

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Address correspondence to Ronald N. Jones, ronald-jones@jmilabs.com.

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**TABLE 1** Key antimicrobial resistance patterns for the 12 monitored nations in the APAC RRS region (26 sites; 5,053 strains)

| Nation (no. of sites/no. of strains) | ESBL (%) | | CARB-R (%)[a] | | | VRE (%) | | MRSA (%) | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | *E. coli* | *Klebsiella* spp. | *Klebsiella* spp. | *P. aeruginosa* | COL/TIG[b] | Rate | VanA | Rate | LZD-S[a] | TIG-S[a] |
| Australia (6/1,136) | 12 | 15 | 0 | 16 | 0/2 | 25 | 0 | 26 | 100 | 100 |
| Hong Kong (1/237) | 46 | 23 | 0 | 17 | 0/0 | 0 | | 28 | 100 | 100 |
| India (5/915) | 78 | 64 | 25 | 32 | 0/2 | 0 | | 45 | 100 | 100 |
| Indonesia (1/175)[f] | 71 | 64 | 0 | 8 | 0/0 | 0 | | 28 | 100 | 100 |
| Japan (4/398)[c] | | | | | | 0 | | 41 | 100 | 100 |
| South Korea (2/462) | 37 | 40 | 0 | 43 | 0/6 | 26 | 80 | 73 | 100 | 100 |
| Malaysia (1/239) | 36 | 45 | 0 | 24 | 0/4 | | | 32 | 100 | 100 |
| New Zealand (2/477) | 11 | 10 | 0 | 6 | 0/0 | 0 | | 9 | 100 | 100 |
| Philippines (1/195)[f] | 47[d] | 55[d] | 5[d] | 50 | 0/5 | 0 | | 59 | 100 | 100 |
| Singapore (1/251) | 21 | 32 | 0 | 22 | 0/4 | | | 52 | 100 | 100 |
| Taiwan (1/137) | 91 | 75 | 10 | 0 | 10/0 | | | | | |
| Thailand (2/431)[f] | 55 | 50 | 5 | 30 | 6/0 | 0 | | 53 | 100 | 100 |
| All (26/5,053) | 60 | 47 | 9 | 26 | 1/2 | 5[e] | 50 | 37 | 100 | 100 |

[a] Abbreviations: R, resistant; S, susceptible.
[b] Among *Klebsiella* strains.
[c] Only Gram-positive cocci were sampled.
[d] Includes two NDM-1 and two IMP-26 strains of *E. coli* and *Klebsiella* spp.
[e] All *Enterococcus faecium* strains in two counties.
[f] RRS study subset.

**TABLE 2** Comparative antimicrobial activities of selected agents tested against key Gram-positive pathogens for the APAC region RRS program (2011)

| Organism (no. of strains tested) and antimicrobial agent | MIC (μg/ml) | | | % S/% R[a] | |
|---|---|---|---|---|---|
| | 50% | 90% | Range | CLSI | EUCAST |
| *S. aureus* (166) | | | | | |
| Ceftriaxone | >8 | >8 | 2–>8 | 48.2/51.8 | 48.2/51.8 |
| Clindamycin | ≤0.25 | >2 | ≤0.25–>2 | 66.3/33.7 | 65.7/33.7 |
| Daptomycin | 0.25 | 0.5 | 0.12–0.5 | 100.0/—[i] | 100.0/0.0 |
| Doxycycline | 0.12 | 8 | ≤0.06–>8 | 71.7/8.4 | 63.3/30.7 |
| Erythromycin | 0.25 | >16 | ≤0.12–>16 | 57.2/38.6 | 58.4/41.6 |
| Levofloxacin | 0.25 | >4 | ≤0.12–>4 | 62.0/36.1 | 62.0/36.1 |
| Linezolid | 1 | 1 | 0.5–2 | 100.0/0.0 | 100.0/0.0 |
| Meropenem | 0.5 | >8 | ≤0.06–>8 | 48.2/51.8 | 48.2/51.8 |
| Oxacillin | >2 | >2 | ≤0.25–>2 | 48.2/51.8 | 48.2/51.8 |
| Teicoplanin | ≤2 | ≤2 | ≤2–8 | 100.0/0.0 | 99.4/0.6 |
| Tigecycline[b] | 0.06 | 0.25 | ≤0.03–0.5 | 100.0/— | 100.0/0.0 |
| Trimethoprim-sulfamethoxazole | ≤0.5 | >4 | ≤0.5–>4 | 88.6/11.4 | 88.6/10.8 |
| Vancomycin | 1 | 1 | 0.5–2 | 100.0/0.0 | 100.0/0.0 |
| CoNS (85)[c] | | | | | |
| Ceftriaxone | >8 | >8 | 1–>8 | 18.8/81.2 | 18.8/81.2 |
| Clindamycin | ≤0.25 | >2 | ≤0.25–>2 | 63.5/31.8 | 63.5/36.5 |
| Daptomycin | 0.5 | 0.5 | 0.12–1 | 100.0/— | 100.0/0.0 |
| Doxycycline | 0.5 | 2 | ≤0.06–>8 | 94.1/1.2 | 74.1/8.2 |
| Erythromycin | >16 | >16 | ≤0.12–>16 | 35.3/64.7 | 35.3/64.7 |
| Levofloxacin | 4 | >4 | ≤0.12–>4 | 42.4/56.5 | 42.4/56.5 |
| Linezolid | 0.5 | 1 | 0.25–1 | 100.0/0.0 | 100.0/0.0 |
| Meropenem | 2 | >8 | ≤0.06–>8 | 18.8/81.2 | 18.8/81.2 |
| Oxacillin | >2 | >2 | ≤0.25–>2 | 18.8/81.2 | 18.8/81.2 |
| Teicoplanin | ≤2 | 4 | ≤2–16 | 95.3/0.0 | 90.6/9.4 |
| Tigecycline[b] | 0.06 | 0.12 | ≤0.03–0.25 | —/— | 100.0/0.0 |
| Trimethoprim-sulfamethoxazole | ≤0.5 | >4 | ≤0.5–>4 | 64.7/35.3 | 64.7/28.2 |
| Vancomycin | 1 | 2 | 0.5–2 | 100.0/0.0 | 100.0/0.0 |
| Enterococci (54)[d] | | | | | |
| Ampicillin | 1 | >8 | 0.5–>8 | 68.5/31.5 | 68.5/31.5 |
| Daptomycin | 1 | 2 | 0.25–4 | 100.0/— | —/— |
| Doxycycline | 8 | >8 | ≤0.06–>8 | 31.5/31.5 | —/— |
| Imipenem | 1 | >8 | 0.25–>8 | —/— | 66.7/33.3 |
| Levofloxacin | >4 | >4 | 0.5–>4 | 44.4/53.7 | —/— |
| Linezolid | 1 | 1 | 0.5–2 | 100.0/0.0 | 100.0/0.0 |
| Teicoplanin | ≤2 | ≤2 | ≤2 | 100.0/0.0 | 100.0/0.0 |
| Tigecycline[b] | 0.06 | 0.06 | ≤0.03–0.12 | 100.0/— | 100.0/0.0 |
| Vancomycin | 1 | 2 | 0.5–2 | 100.0/0.0 | 100.0/0.0 |
| *S. pneumoniae* (42)[e] | | | | | |
| Amoxicillin-clavulanate | ≤1 | 8 | ≤1–>8 | 76.2/21.4 | —/— |
| Ceftriaxone | ≤0.06 | 8 | ≤0.06–8 | 78.6/14.3 | 66.7/14.3 |
| Clindamycin | ≤0.25 | >2 | ≤0.25–>2 | 50.0/50.0 | 50.0/50.0 |
| Erythromycin | 1 | >16 | ≤0.12–>16 | 47.6/52.4 | 47.6/52.4 |
| Levofloxacin | 1 | 1 | 0.5–2 | 100.0/0.0 | 100.0/0.0 |
| Linezolid | 0.5 | 1 | 0.25–1 | 100.0/— | 100.0/0.0 |
| Penicillin[f] | ≤0.06 | 4 | ≤0.06–8 | 76.2/4.8 | 66.7/23.8 |
| Tetracycline | >8 | >8 | ≤0.25–>8 | 28.6/69.0 | 28.6/71.4 |
| Tigecycline[b] | ≤0.03 | ≤0.03 | ≤0.03–0.06 | 100.0/— | —/— |
| Trimethoprim-sulfamethoxazole | ≤0.5 | >4 | ≤0.5–>4 | 50.0/40.5 | 57.1/40.5 |
| Vancomycin | 0.25 | 0.5 | 0.25–0.5 | 100.0/— | 100.0/0.0 |
| Beta-hemolytic streptococci (27)[g] | | | | | |
| Ceftriaxone | ≤0.06 | 0.12 | ≤0.06–0.25 | 100.0/— | 100.0/0.0 |
| Clindamycin | ≤0.25 | >2 | ≤0.25–>2 | 66.7/33.3 | 66.7/33.3 |
| Daptomycin | 0.12 | 0.25 | ≤0.06–0.5 | 100.0/— | 100.0/0.0 |
| Erythromycin | ≤0.12 | >16 | ≤0.12–>16 | 55.6/37.0 | 55.6/37.0 |

(Continued on following page)

**TABLE 2** (Continued)

| Organism (no. of strains tested) and antimicrobial agent | MIC (μg/ml) | | | % S/% R[a] | |
|---|---|---|---|---|---|
| | 50% | 90% | Range | CLSI | EUCAST |
| Levofloxacin | 0.5 | 1 | 0.25–>4 | 96.3/3.7 | 92.6/3.7 |
| Linezolid | 1 | 1 | 0.5–1 | 100.0/— | 100.0/0.0 |
| Penicillin | ≤0.06 | ≤0.06 | ≤0.06 | 100.0/— | 100.0/0.0 |
| Tetracycline | >8 | >8 | ≤0.25–>8 | 14.8/81.5 | 14.8/85.2 |
| Tigecycline[b] | ≤0.03 | 0.12 | ≤0.03–0.12 | 100.0/— | 100.0/0.0 |
| Trimethoprim-sulfamethoxazole | ≤0.5 | ≤0.5 | ≤0.5 | —/— | 100.0/0.0 |
| Vancomycin | 0.5 | 0.5 | 0.25–1 | 100.0/— | 100.0/0.0 |
| Viridans group streptococci (10)[h] | | | | | |
| Ceftriaxone | 0.25 | 1 | 0.12–4 | 90.0/10.0 | 80.0/20.0 |
| Clindamycin | ≤0.25 | >2 | ≤0.25–>2 | 80.0/20.0 | 80.0/20.0 |
| Daptomycin | 0.5 | 1 | 0.12–1 | 100.0/— | —/— |
| Erythromycin | ≤0.12 | >16 | ≤0.12–>16 | 50.0/50.0 | —/— |
| Levofloxacin | 1 | 1 | 0.25–2 | 100.0/0.0 | —/— |
| Linezolid | 0.5 | 1 | 0.5–1 | 100.0/— | —/— |
| Penicillin | 0.12 | 0.5 | ≤0.06–4 | 50.0/10.0 | 60.0/10.0 |
| Tetracycline | 8 | >8 | 0.5–>8 | 40.0/60.0 | —/— |
| Tigecycline[b] | ≤0.03 | ≤0.03 | ≤0.03–0.25 | 100.0/— | —/— |
| Vancomycin | 0.5 | 0.5 | 0.25–1 | 100.0/— | 100.0/0.0 |

[a] Criteria as published by the CLSI (2) and EUCAST (11); β-lactam susceptibility against staphylococci should be directed by the oxacillin test results.
[b] U.S. FDA breakpoints were applied when available (12).
[c] Includes *Staphylococcus epidermidis* (three strains), *Staphylococcus haemolyticus* (one strain), *Staphylococcus hominis* (one strain), *Staphylococcus warneri* (two strains), and coagulase-negative staphylococci not identified to species level (78 strains).
[d] Includes *Enterococcus avium* (one strain), *E. faecalis* (35 strains), and *Enterococcus faecium* (18 strains).
[e] 33.3% penicillin nonsusceptible at ≥0.12 μg/ml.
[f] Criteria as published by the CLSI (2) for "Penicillin parenteral (nonmeningitis)."
[g] Includes *Streptococcus dysgalactiae* (six strains), group A *Streptococcus* (five strains), group B *Streptococcus* (11 strains), group F *Streptococcus* (one strain), group G *Streptococcus* (three strains), and beta-hemolytic streptococci not identified to species level (one strain).
[h] Includes *Streptococcus mitis* (one strain), *Streptococcus oralis* (one strain), *Streptococcus salivarius* (one strain), *Streptococcus sanguinis* (one strain), and viridans group streptococci not identified to species level (six strains).
[i] —, no interpretation.

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The APAC region historically has had among the highest levels of resistance for many Gram-positive pathogens (methicillin-resistant *Staphylococcus aureus* [MRSA], vancomycin-resistant enterococci [VRE], penicillin-resistant pneumococci, and fluoroquinolone-resistant streptococci) (5–7) and Gram-negative bacilli (extended-spectrum β-lactamase [ESBL]-producing *Enterobacteriaceae* and multidrug-resistant [MDR] nonfermentative species) (5, 8–10). However, the resistance rates among nations within the region can be diverse, being generally lower in Japan and Australia/New Zealand and more elevated in eastern Asia and the Asian subcontinent countries. The results for 12 nations are presented in Table 1, and more detailed analysis of the APAC RRS sites is provided in Tables 2 and 3.

A total of 5,053 strains were processed from the APAC region in 2011, with a distribution of 137 isolates from Taiwan to 1,136 samples from Australia (26 sites or hospital laboratories overall). These organisms were from unique clinical specimens recognized as true infections. The distribution of samples from hospitalized patients was as follows: *S. aureus*, 1,046; *Streptococcus pneumoniae*, 419; beta-hemolytic streptococci (βHS), 286; viridans group streptococci (VGS), 183; *Escherichia coli*, 501; *Pseudomonas aeruginosa*, 430; *Klebsiella* spp., 361; and *Acinetobacter* spp., 243. The supplemental subset of RRS site strains is separately tabulated in Tables 2 and 3.

Commonly marketed agents such as linezolid (LZD), vancomycin (VAN), tigecycline (TIG), colistin (COL), piperacillin-tazobactam (P/T), cefoperazone-sulbactam (C/S), amikacin (AMK), levofloxacin (LEV), and carbapenems were tested. Isolates were mainly from bloodstream, respiratory tract, and skin/skin structure infections (17, 28, and 17%, respectively). Susceptibility to over 30 antimicrobial agents was determined by reference broth microdilution methods as described by the Clinical and Laboratory Standards Institute (1). Quality control (QC) strains (*S. aureus* ATCC 25923 and ATCC 29213, *Enterococcus faecalis* ATCC 29212, *S. pneumoniae* ATCC 49619, *E. coli* ATCC 25922 and ATCC 35218, and *P. aeruginosa* ATCC 27853) were tested concurrently, and all QC values were observed within CLSI (2) control ranges. Susceptibility interpretive criteria from the CLSI (2), EUCAST (11), and U.S. FDA (12) were applied.

Screening tests for ESBL-phenotype strains were determined using CLSI-recommended breakpoints of ≥2 μg/ml for ceftriaxone, ceftazidime, or aztreonam (2). Carbapenem-nonsusceptible concentrations were ≥2 μg/ml for doripenem, imipenem, or meropenem when testing *Enterobacteriaceae* (carbapenem-resistant *Enterobacteriaceae* [CRE]) and ≥4 μg/ml for doripenem, imipenem, or meropenem when *P. aeruginosa* strains were processed for carbapenem-resistant (CARB-R) strains. Organisms meeting these criteria were further tested by the Check-MDR CT101 kit (Wageningen, The Netherlands) and microarray method to determine β-lactamase genes, and selected isolates had gene sequencing performed. Furthermore, methods as described by Mendes et al. (13) were applied to the testing for resistance mechanisms in sampled pathogens, and potential clonality was assessed by pulsed-field gel electrophoresis (PFGE).

**TABLE 3** Multidrug comparisons of antimicrobial activity when testing Gram-negative pathogens in the RRS program sites for the APAC region (2011)

| Organism (no. of strains tested) and antimicrobial agent | MIC (μg/ml) | | | % S/% R[a] | |
|---|---|---|---|---|---|
| | 50% | 90% | Range | CLSI | EUCAST |
| *E. coli* (all; 101) | | | | | |
| Amikacin | 4 | 16 | 1–>32 | 95.0/5.0 | 89.0/5.0 |
| Ampicillin-sulbactam | 16 | >32 | 1–>32 | 30.7/44.6 | 30.7/69.3 |
| Cefepime | 8 | >16 | ≤0.5–>16 | 55.4/36.6 | 48.5/50.5 |
| Cefoperazone | >32 | >32 | ≤0.25–>32 | 44.0/54.0 | —[h]/— |
| Cefoperazone-sulbactam[b] | 4 | 16 | ≤0.25–>32 | 91.1/2.0 | —/— |
| Ceftazidime | 4 | 32 | 0.06–>32 | 52.5/44.6 | 41.6/47.5 |
| Ceftriaxone | >8 | >8 | ≤0.06–>8 | 40.6/59.4 | 40.6/59.4 |
| Colistin | 0.5 | 0.5 | ≤0.25–>4 | —/— | 98.0/2.0 |
| Gentamicin | 2 | >8 | ≤1–>8 | 56.4/42.6 | 56.4/43.6 |
| Imipenem | ≤0.12 | 0.25 | ≤0.12–8 | 97.0/1.0 | 99.0/0.0 |
| Levofloxacin | >4 | >4 | ≤0.12–>4 | 37.6/59.4 | 37.6/62.4 |
| Meropenem | ≤0.06 | ≤0.06 | ≤0.06–>8 | 97.0/3.0 | 97.0/2.0 |
| Piperacillin-tazobactam | 2 | 16 | ≤0.5–>64 | 91.1/3.0 | 82.2/8.9 |
| Tetracycline | >8 | >8 | 0.5–>8 | 29.7/70.3 | —/— |
| Tigecycline[c] | 0.12 | 0.25 | ≤0.03–2 | 100.0/0.0 | 99.0/0.0 |
| Tobramycin | 4 | >16 | 0.5–>16 | 51.5/44.6 | 49.5/48.5 |
| Trimethoprim-sulfamethoxazole | >4 | >4 | ≤0.5–>4 | 35.6/64.4 | 35.6/63.4 |
| ESBL phenotype (61)[d] | | | | | |
| Amikacin | 4 | 16 | 2–>32 | 91.8/8.2 | 83.6/8.2 |
| Cefoperazone-sulbactam[b] | 8 | 32 | ≤0.25–>32 | 85.2/3.3 | —/— |
| Colistin | 0.5 | 0.5 | ≤0.25–>4 | —/— | 96.7/3.3 |
| Imipenem | ≤0.12 | 0.25 | ≤0.12–8 | 95.1/1.6 | 98.4/0.0 |
| Meropenem | ≤0.06 | ≤0.06 | ≤0.06–>8 | 95.1/4.9 | 95.1/3.3 |
| Piperacillin-tazobactam | 4 | 32 | 1–>64 | 85.2/4.9 | 73.8/14.8 |
| Tigecycline[c] | 0.12 | 0.12 | ≤0.03–2 | 100.0/0.0 | 98.4/0.0 |
| *Klebsiella* spp. (all; 75)[e] | | | | | |
| Amikacin | 2 | 8 | 0.5–>32 | 97.3/2.7 | 96.0/2.7 |
| Ampicillin-sulbactam | 8 | >32 | 0.5–>32 | 50.7/40.0 | 50.7/49.3 |
| Cefepime | ≤0.5 | >16 | ≤0.5–>16 | 65.3/30.7 | 57.3/37.3 |
| Cefoperazone | 1 | >32 | ≤0.25–>32 | 57.3/41.3 | —/— |
| Cefoperazone-sulbactam[b] | 1 | 32 | ≤0.25–>32 | 88.0/4.0 | —/— |
| Ceftazidime | 0.25 | >32 | 0.06–>32 | 65.3/30.7 | 58.7/34.7 |
| Ceftriaxone | 0.12 | >8 | ≤0.06–>8 | 53.3/46.7 | 53.3/46.7 |
| Colistin | 0.5 | 0.5 | ≤0.25–4 | —/— | 98.7/1.3 |
| Gentamicin | ≤1 | >8 | ≤1–>8 | 66.7/33.3 | 66.7/33.3 |
| Imipenem | ≤0.12 | 0.5 | ≤0.12–8 | 96.0/4.0 | 96.0/0.0 |
| Levofloxacin | ≤0.12 | >4 | ≤0.12–>4 | 84.0/12.0 | 81.3/16.0 |
| Meropenem | ≤0.06 | ≤0.06 | ≤0.06–>8 | 94.7/5.3 | 94.7/4.0 |
| Piperacillin-tazobactam | 4 | 64 | ≤0.5–>64 | 81.3/8.0 | 72.0/18.7 |
| Tetracycline | 2 | >8 | 0.5–>8 | 60.0/40.0 | —/— |
| Tigecycline[c] | 0.25 | 1 | 0.12–4 | 98.7/0.0 | 92.0/1.3 |
| Tobramycin | 0.5 | >16 | 0.25–>16 | 65.3/32.0 | 58.7/34.7 |
| Trimethoprim-sulfamethoxazole | ≤0.5 | >4 | ≤0.5–>4 | 54.7/45.3 | 54.7/42.7 |
| ESBL phenotype (35)[d] | | | | | |
| Amikacin | 4 | 8 | 1–>32 | 94.3/5.7 | 91.4/5.7 |
| Cefoperazone-sulbactam[b] | 8 | 32 | ≤0.25–>32 | 74.3/8.6 | —/— |
| Colistin | 0.5 | 2 | ≤0.25–4 | —/— | 97.1/2.9 |
| Imipenem | ≤0.12 | 1 | ≤0.12–8 | 91.4/8.6 | 91.4/0.0 |
| Levofloxacin | 0.5 | >4 | ≤0.12–>4 | 65.7/25.7 | 60.0/34.3 |
| Meropenem | ≤0.06 | 4 | ≤0.06–>8 | 88.6/11.4 | 88.6/8.6 |
| Piperacillin-tazobactam | 16 | >64 | 2–>64 | 60.0/17.1 | 42.9/40.0 |
| Tigecycline[c] | 0.5 | 2 | 0.12–4 | 97.1/0.0 | 85.7/2.9 |
| *Enterobacter* spp. (36)[f] | | | | | |
| Amikacin | 2 | 8 | 1–16 | 100.0/0.0 | 97.2/0.0 |
| Cefepime | 4 | >16 | ≤0.5–>16 | 61.1/36.1 | 38.9/47.2 |
| Cefoperazone-sulbactam[b] | 8 | >32 | ≤0.25–>32 | 83.3/11.1 | —/— |

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**TABLE 3** (Continued)

| Organism (no. of strains tested) and antimicrobial agent | MIC (μg/ml) | | | % S/% R[a] | |
|---|---|---|---|---|---|
| | 50% | 90% | Range | CLSI | EUCAST |
| Colistin | 0.5 | >4 | ≤0.25–>4 | —/— | 75.0/25.0 |
| Gentamicin | 4 | >8 | ≤1–>8 | 50.0/47.2 | 44.4/50.0 |
| Imipenem | 0.25 | 1 | ≤0.12–2 | 94.4/0.0 | 100.0/0.0 |
| Levofloxacin | 0.5 | >4 | ≤0.12–>4 | 77.8/19.4 | 69.4/22.2 |
| Meropenem | ≤0.06 | 0.12 | ≤0.06–0.5 | 100.0/0.0 | 100.0/0.0 |
| Piperacillin-tazobactam | 16 | >64 | 1–>64 | 55.6/19.4 | 47.2/44.4 |
| Tetracycline | 2 | >8 | 0.5–>8 | 52.8/44.4 | —/— |
| Tigecycline[c] | 0.25 | 2 | 0.12–4 | 91.7/0.0 | 88.9/8.3 |
| Trimethoprim-sulfamethoxazole | ≤0.5 | >4 | ≤0.5–>4 | 52.8/47.2 | 52.8/47.2 |
| *P. aeruginosa* (60) | | | | | |
| Amikacin | 4 | 16 | 0.5–>32 | 91.7/6.7 | 88.3/8.3 |
| Cefepime | 4 | >16 | 1–>16 | 71.7/18.3 | 71.7/28.3 |
| Cefoperazone-sulbactam[b] | 8 | >32 | 1–>32 | 66.7/11.7 | —/— |
| Cefoperazone | 8 | >32 | 2–>32 | 61.7/35.0 | —/— |
| Ceftazidime | 4 | >32 | 1–>32 | 70.0/28.3 | 70.0/30.0 |
| Colistin | 2 | 2 | 1–4 | 98.3/0.0 | 98.3/1.7 |
| Gentamicin | 2 | >8 | ≤1–>8 | 85.0/13.3 | 85.0/15.0 |
| Imipenem | 1 | >8 | 0.5–>8 | 71.7/28.3 | 71.7/13.3 |
| Levofloxacin | 0.5 | >4 | ≤0.12–>4 | 75.0/20.0 | 61.7/25.0 |
| Meropenem | 0.25 | 8 | ≤0.06–>8 | 71.7/21.7 | 71.7/10.0 |
| Piperacillin-tazobactam | 8 | >64 | 1–>64 | 66.7/16.7 | 66.7/33.3 |
| Tobramycin | 0.5 | 16 | 0.25–>16 | 85.0/13.3 | 85.0/15.0 |
| *Acinetobacter* spp. (38)[g] | | | | | |
| Amikacin | 16 | >32 | 0.5–>32 | 50.0/50.0 | 47.4/50.0 |
| Cefoperazone-sulbactam[b] | 16 | >32 | 0.5–>32 | 55.3/26.3 | —/— |
| Colistin | 1 | 2 | 0.5–>4 | 97.4/2.6 | 97.4/2.6 |
| Tigecycline | 1 | 2 | ≤0.03–4 | —/— | —/— |

[a] Criteria as published by the CLSI (2) and EUCAST (11).
[b] Criteria as published by the CLSI (2) for cefoperazone used for cefoperazone-sulbactam.
[c] U.S. FDA breakpoints were applied when available (12).
[d] Only drugs with ≥40% susceptibility are listed.
[e] Includes *Klebsiella oxytoca* (three strains), *Klebsiella pneumoniae* (53 strains), and *Klebsiella* spp. not identified to species level (19 strains).
[f] Includes *Enterobacter aerogenes* (five strains), *Enterobacter cloacae* (24 strains), *Enterobacter sakazakii* (one strain), and *Enterobacter* spp. not identified to species level (six strains).
[g] Only drugs active against ≥50% of strains are shown.
[h] —, no interpretation.

Table 1 provides a general overview of key antimicrobial resistances (CLSI criteria) among the 12 monitored nations (three were RRS program countries). These data revealed that (i) ESBL rates for *E. coli/Klebsiella* spp. ranged from 11%/10% (New Zealand) to 91%/75% (Taiwan) (overall APAC average, 60%/47%); (ii) CARB-R rates for *Klebsiella* spp. ranged from 0% (seven nations) to 25% (India) (APAC average, 9%), with colistin and tigecycline activity being highest (90 to 100% susceptible rate); (iii) *P. aeruginosa* CARB-R was 26% overall, highest in Philippines (50%); (iv) VRE isolates were generally rare (5% overall) outside Australia and South Korea; and (v) MRSA rates (37% overall) ranged widely from 9% (New Zealand) to 73% (South Korea).

Of note, four CARB-R strains were noted in a medical center in Philippines that revealed carbapenemases. These included two *E. coli* strains with NDM-1 (8, 14), another *E. coli* strain with IMP-26, and a *K. pneumoniae* strain also with IMP-26. These strains occurred among a population of *E. coli* and *Klebsiella* strains that had a high ESBL-phenotype rate of 47 to 60% (Tables 1 and 3). Clonal spread of these strains was documented by PFGE.

Table 2 shows the RRS site results for Gram-positive pathogens in the supplemental nations. Key observations among these strains were that (i) the MRSA rate was nearly 52.0%, but daptomycin, glycopeptides, linezolid, and tigecycline inhibited all strains at CLSI (2) or U.S. FDA (12) susceptible breakpoints; (ii) a significant number (9.4%) of coagulase-negative staphylococcus (CoNS) strains were teicoplanin resistant using EUCAST (11) breakpoints; (iii) no VRE (CLSI criteria) were noted in the three countries; (iv) macrolide-, clindamycin-, tetracycline-, and levofloxacin-resistant (3.7%; CLSI) beta-hemolytic streptococci were detected; (v) ceftriaxone resistance (CLSI) in the pneumococci was high (14.3%); and (vi) glycopeptides, linezolid, and tigecycline were the most potent antimicrobials tested against the Gram-positive cocci.

Table 3 lists the dominantly cultured Gram-negative pathogens (310 strains, including 96 ESBL-phenotype isolates) in the Indonesia, Philippines, and Thailand collections. The ESBL-phenotype rate in *E. coli* was 59.4% (APAC regional rate, 48.0%), highest for Indonesia at 71.0%. Also, the ESBL-phenotype rate in *Klebsiella* was elevated (46.7%) and equal to that observed for the region (47.0%, Table 1); again, the highest rate occurred among Indonesia samples at 64.0%. Amikacin, carbapenems (imipenem or meropenem), colistin, and tigecycline had the best coverage (percent susceptible) of the ESBL-producing isolate subsets (Table 3).

Few potent agents with broad coverage of *P. aeruginosa* were noted, the best being amikacin (88.3 to 91.7% susceptible, CLSI and EUCAST criteria), colistin (98.3%), gentamicin (85.0%), and tobramycin (85.0%). The CARB-nonsusceptible rate was 28.3%. *Acinetobacter* spp. were even more refractory to available drugs, having the lowest $MIC_{50/90}$ values (1/2 μg/ml, respectively) for colistin and tigecycline (Table 3).

As documented here for the 2011 surveillance year, some problems continue to emerge in previously unaffected or unsampled nations, and the prevalence of various resistance mechanisms (β-lactamase-mediated types) continues to escalate (Table 1). Lower levels of ESBL and CARB-R profiles occur in Australia and New Zealand; in contrast, India, Indonesia, and Taiwan have rates greater than the all-APAC average and for most nations in western Europe and the United States (15, 16). The APAC region has also been the geographic area associated with therapy-compromising new enzymes (e.g., NDM-1), limiting use of the important carbapenem class of β-lactams (4, 8, 14). In this study, metallo-β-lactamase (MBL)-producing strains were easily identified, including two NDM-1 *E. coli* strains from a medical center with other IMP-series enzymes. Furthermore, Bonnet (9) and others have noted that CTX-M-series enzymes have become the dominant ESBL type in this region as well as in China (17), also found here (data not shown). Few drugs have been identified as candidates to treat infections caused by these MDR pathogens.

Although MRSA rates average 37.0% (range, 9.0 to 73.0% [Table 1]), the results remain consistent with other areas of the world and on average less than that documented in the United States (18). Several high-quality antimicrobials remain for therapy of MDR Gram-positive coccus infections, especially glycopeptides and lipopeptides (daptomycin), oxazolidinones (linezolid), some tetracyclines, and their derivative tigecycline (Tables 1 and 2) (3, 5–7, 18, 19).

Surveillance of APAC area nations will be critical to understanding of resistance emergence, spread, and impact on the greatest proportion of the world's population (China, India, and Indonesia), and the delivery of quality antimicrobial care must be a priority of public health over the next decade. To maximize favorable clinical outcomes and to preserve the utility of the currently available agents, drug stewardship and the rapid development of new antimicrobials should be the paramount focus of governmental regulators and the pharmaceutical industry (10).

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